



Figure 1

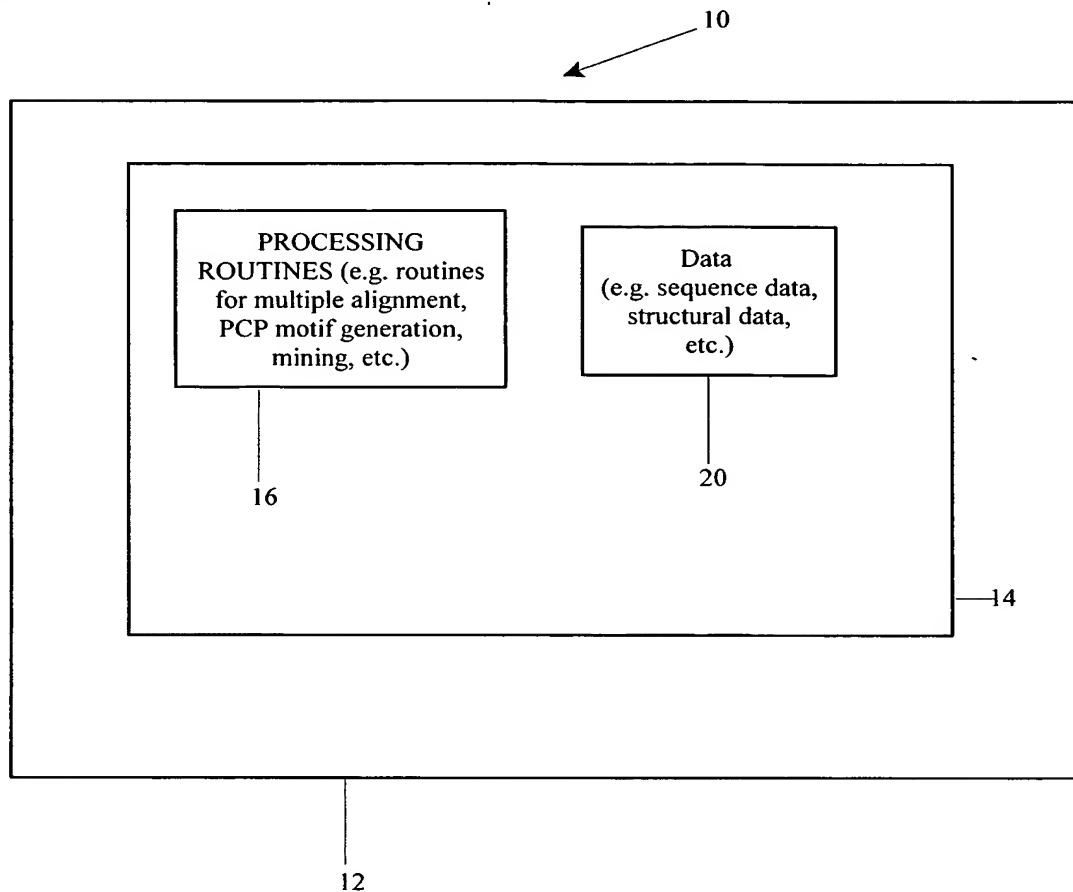


Figure 2

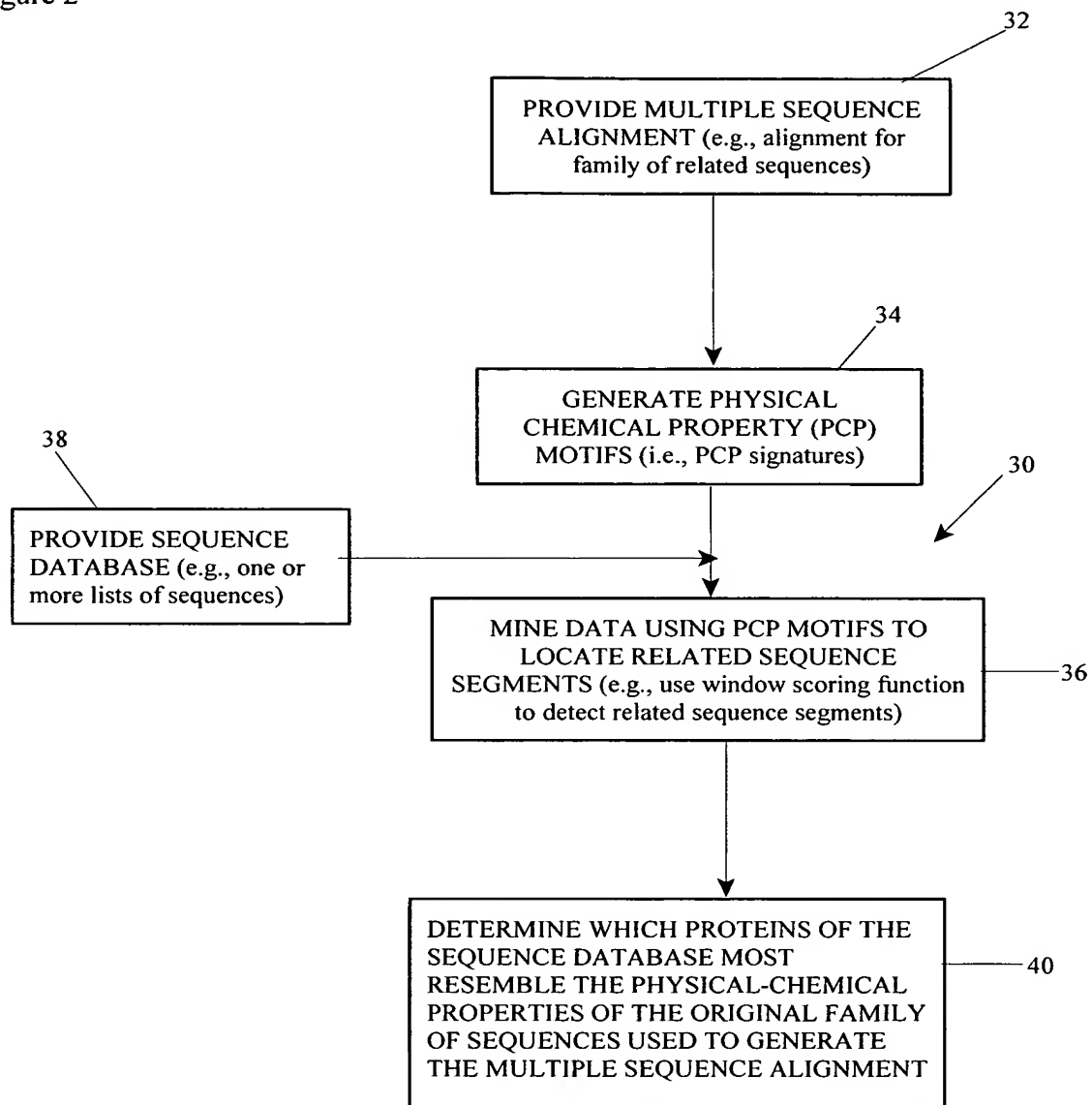
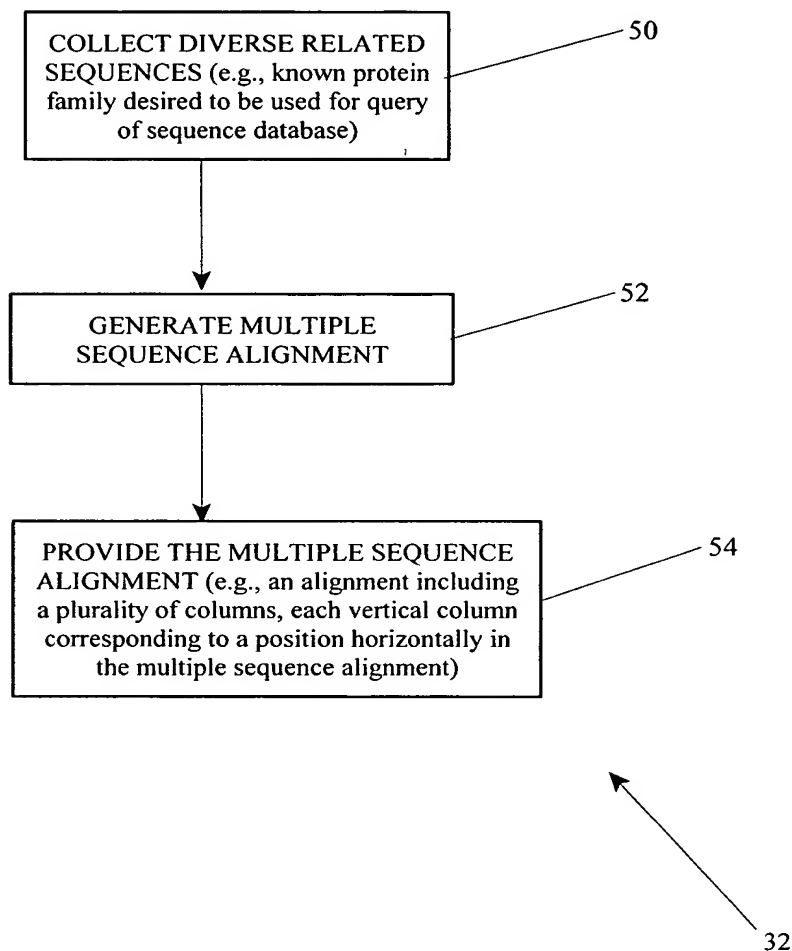


Figure 3



REPLACEMENT SHEET

Figure 4

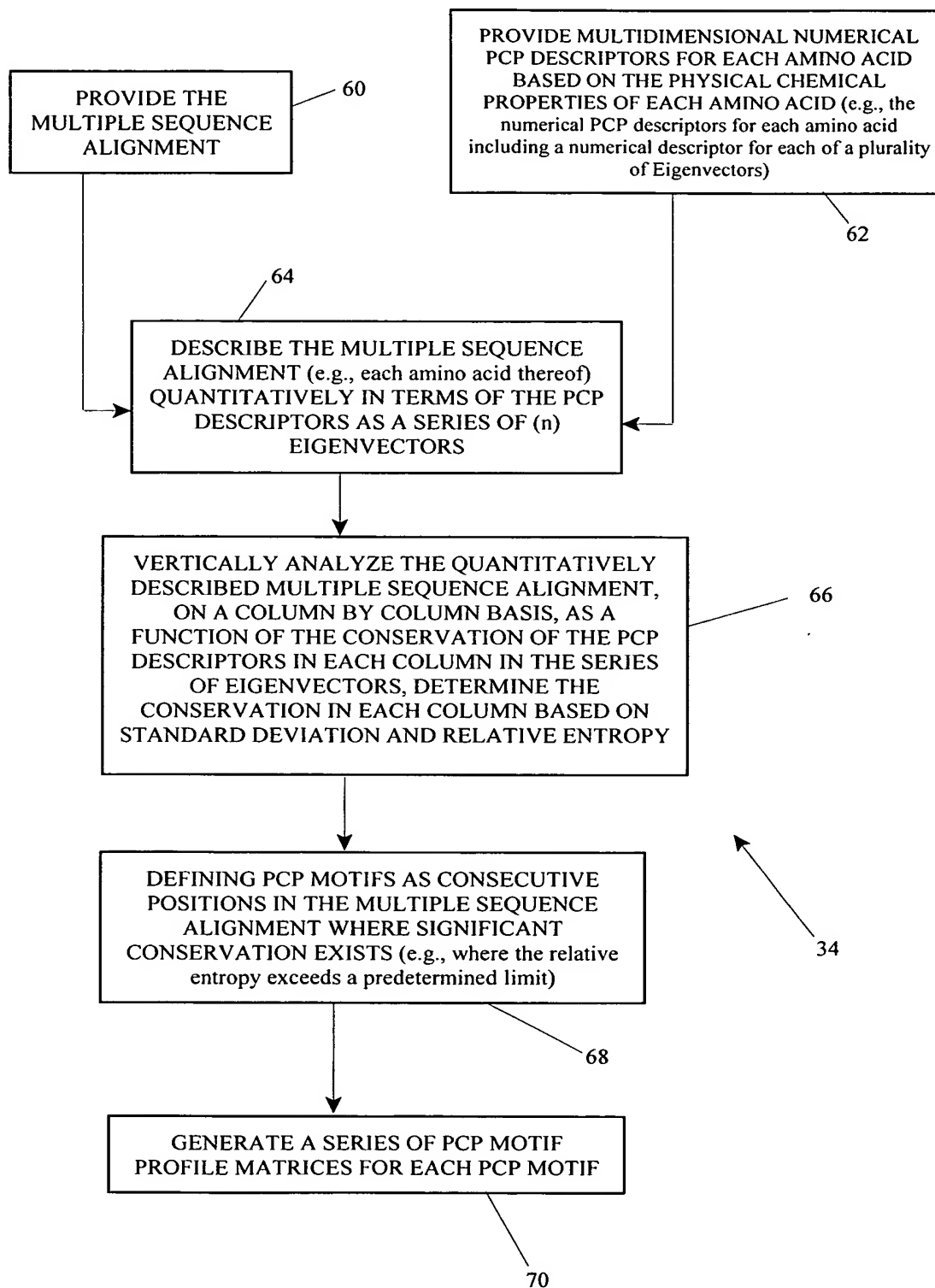


Figure 5

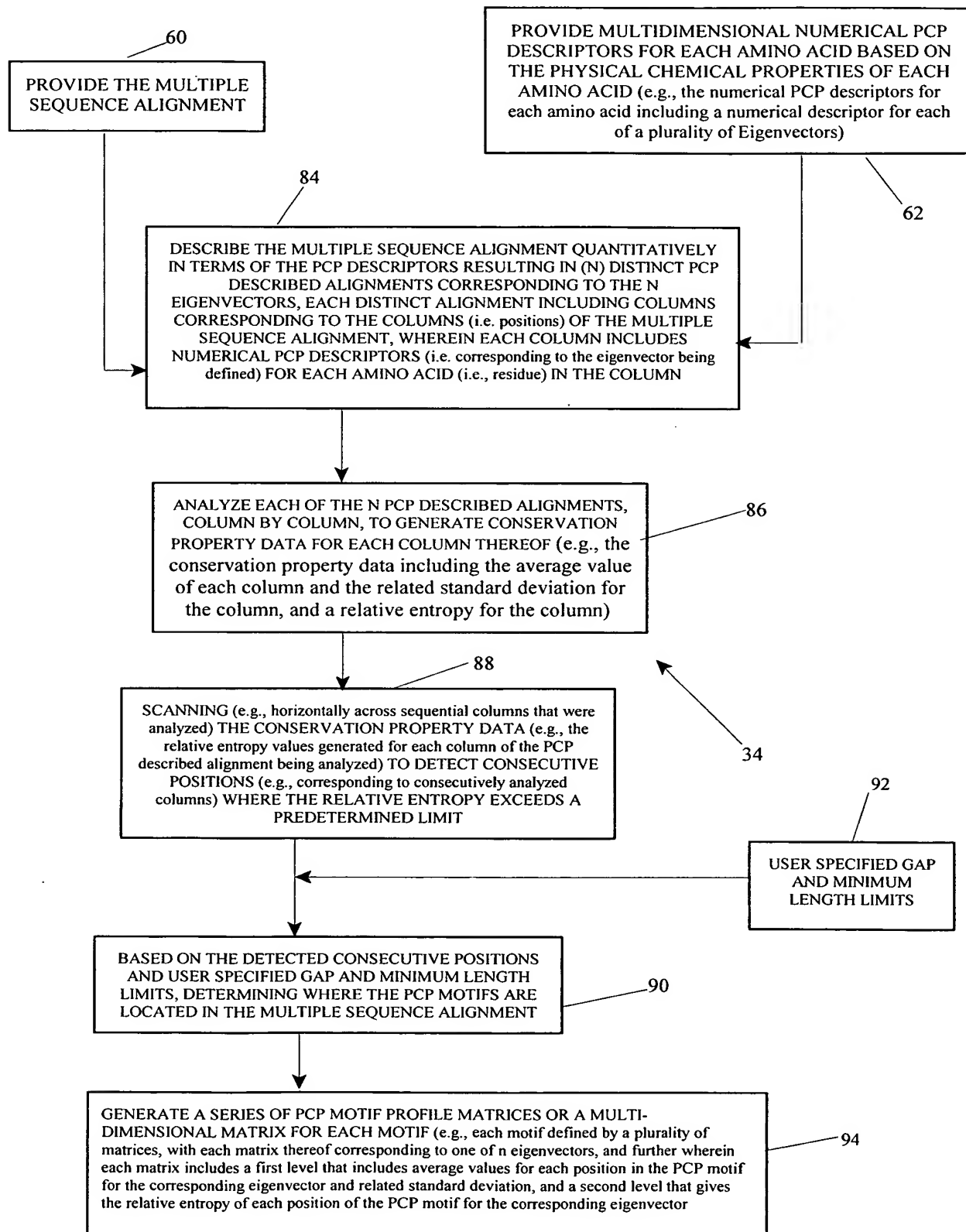


Figure 6

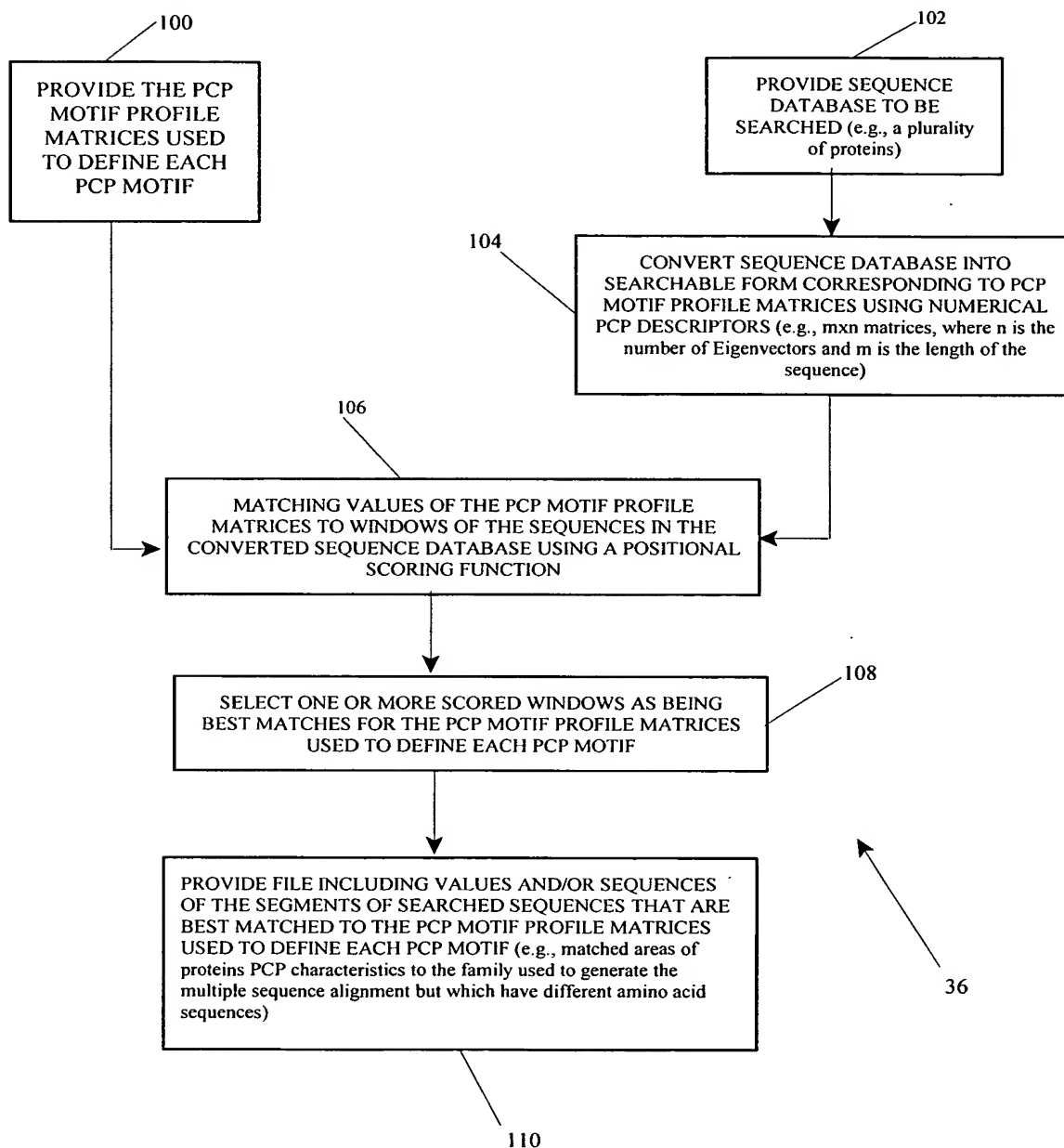


Figure 7

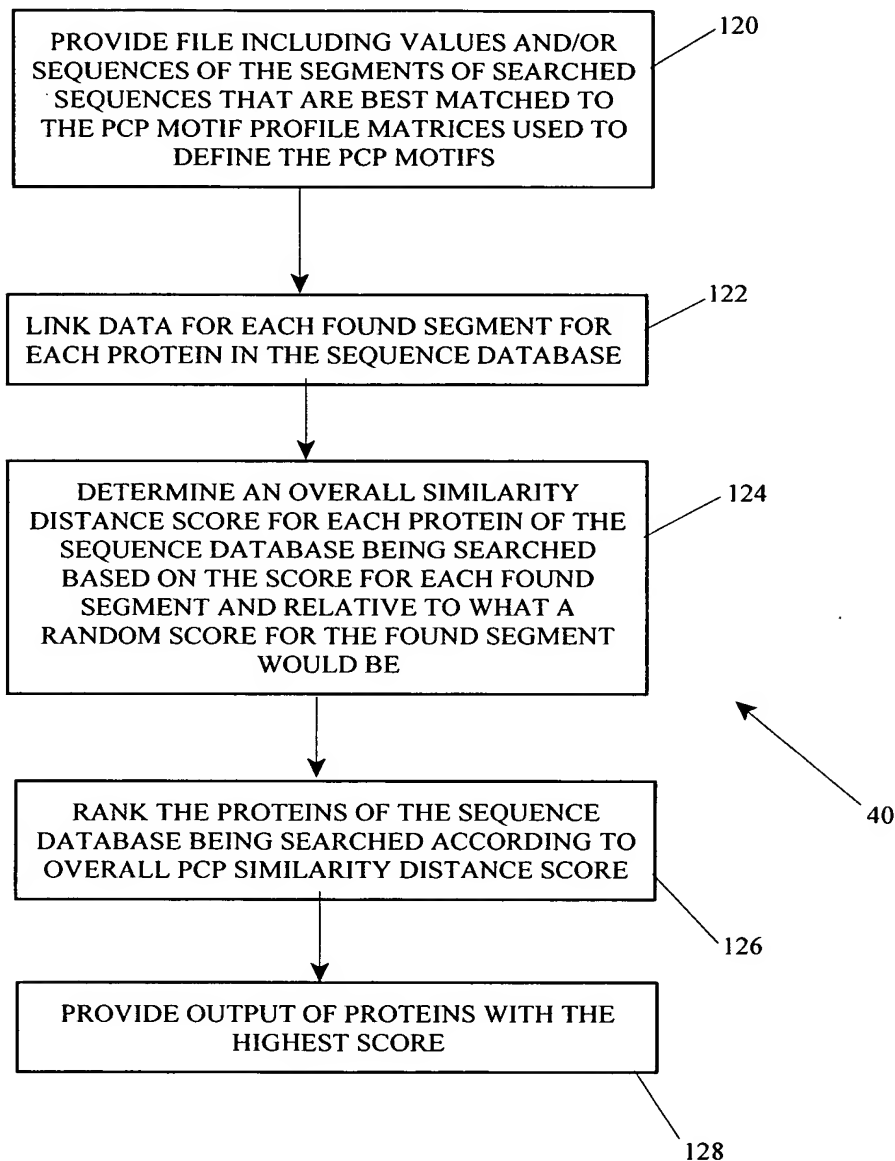


Figure 8

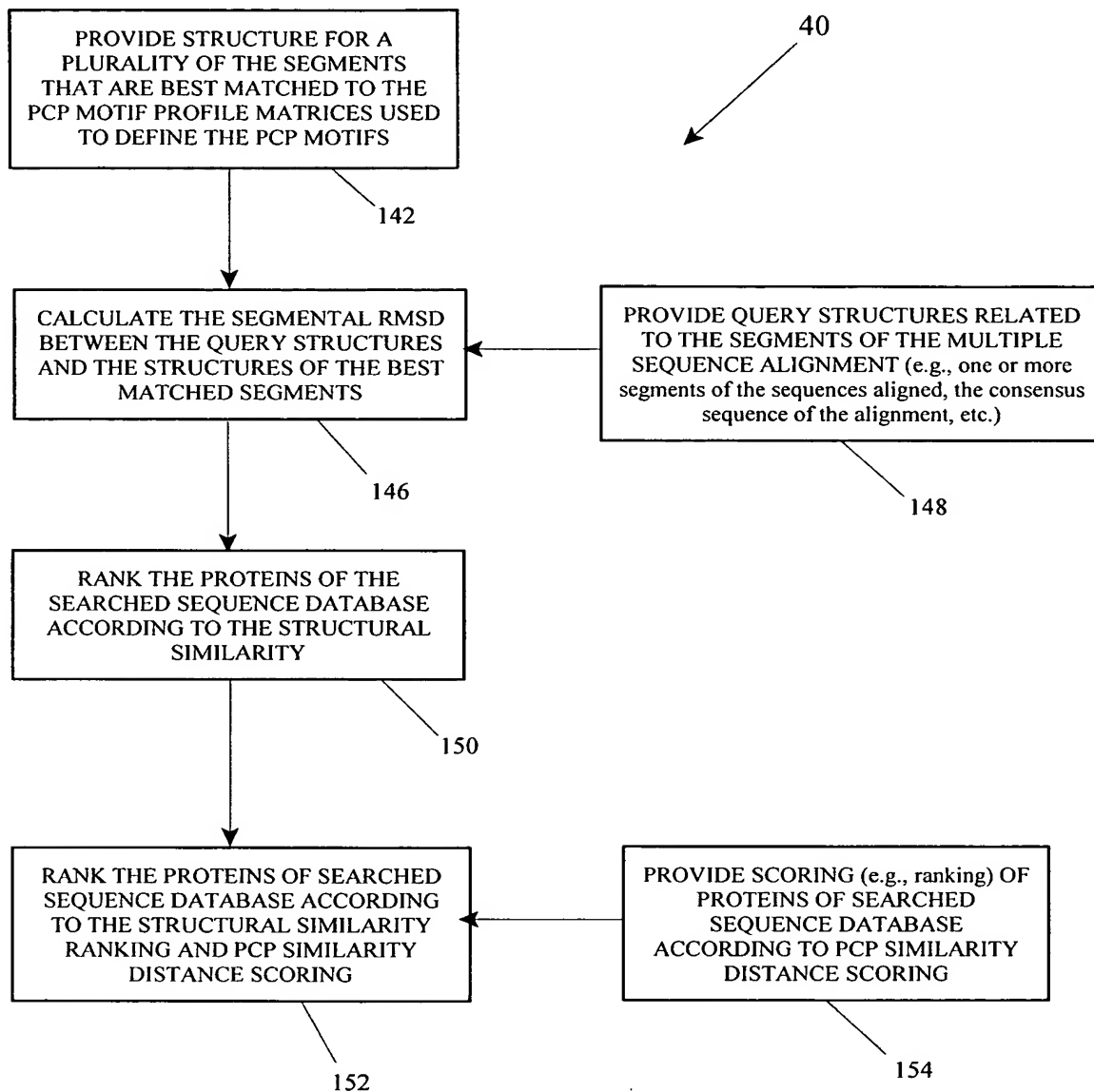




Figure 9A

Motif No.	Query sequence (human APE)	(S1)	(S2)	(S3)	(S4)	42 APE score ave. $\pm$ std. dev	ASTRAL40 ave. $\pm$ std. dev
1	62LKICSWNVVDGLRA 74	0.91*	0.90*	0.63*	0.73*	0.87 $\pm$ 0.05	0.56 $\pm$ 0.05
2	89PDILCLQETK 98	0.96*	0.93*	0.84*	0.70*	0.92 $\pm$ 0.04	0.61 $\pm$ 0.07
3	125 KEGYSGVGLLSRQCP 139	0.91*	0.86*	0.60	0.66	0.85 $\pm$ 0.06	0.64 $\pm$ 0.05
4	145 GIGDEEHDQEGRVIVAEFDSFVL 169	0.94*	0.77*	0.71	0.81	0.84 $\pm$ 0.09	0.67 $\pm$ 0.07
5	171 YVPNA 175	0.96*	0.96*	0.68	0.86	0.94 $\pm$ 0.06	0.68 $\pm$ 0.13
6	181 RLEYRQRW 188	0.80*	0.70*	0.78	0.77	0.74 $\pm$ 0.06	0.67 $\pm$ 0.05
7	204 PLVLCGDLNVAH 215	0.96*	0.88*	0.82*	0.78*	0.90 $\pm$ 0.04	0.55 $\pm$ 0.08
8	231 GFTPQERQFGEL 243	0.96*	0.91*	0.78	0.73	0.87 $\pm$ 0.09	0.70 $\pm$ 0.07
9	247 VPLADSR 254	0.96*	0.93*	0.70	0.83	0.91 $\pm$ 0.08	0.74 $\pm$ 0.11
10	264 YTFWTYM 270	0.86*	0.77*	0.61	0.70	0.84 $\pm$ 0.08	0.61 $\pm$ 0.06
11	274 RSKNVGWRLDYFLLSHSL 291	0.92*	0.89*	0.56	0.64	0.90 $\pm$ 0.04	0.54 $\pm$ 0.07
12	306 GSDHCPI 312	0.93*	0.94*	0.88*	0.83*	0.92 $\pm$ 0.03	0.52 $\pm$ 0.09

# REPLACEMENT SHEET

Figure 9B

PDB <sup>1</sup>	Score in bits (fraction to the highest score)	Motifs found	SCOP <sup>2</sup>	EC <sup>3</sup>	Description
1HD7	1942 (1.00)	1,2,3,4,5,6,7,8,9,10,11,12	d.151.1.1	4.2.99.18	APE
1AKO	1861 (0.96)	1,2,3,4,5,7,8,9,10,11,12	d.151.1.1	3.1.11.2	Exonuclease III
2DNJ	1094 (0.56)	2,6,7,12	d.151.1.1	0.0.0.0	Deoxyribonuclease I
119Y	1056 (0.54)	1,4,5,6,7,9,12	d.151.1.2	0.0.0.0	Phosphatidylinositol phosphate Synaptotjanin
1B3U	840 (0.43)	5,7,9,12	a.118.1.2	0.0.0.0	Regulatory domain of protein phosphatase
1MDA	814 (0.42)	6,9,11,12	b.69.2.1	1.4.99.3	Methylamine dehydrogenase
1MPY	797 (0.41)	7,9,12	d.32.1.3	1.13.11.2	Catechol 2,3-dioxygenase
1EKM	792 (0.41)	6,7,12	b.30.2.1	1.4.3.6	Copper amine oxidase
1YRG	737 (0.38)	2,9,12	c.10.1.2	0.0.0.0	GTPase RNA1
1QQ9	698 (0.36)	5,6,12	c.56.5.4	3.4.11.-	Aminopeptidase

<sup>1</sup>PDB code of the protein

<sup>2</sup>SCOP code and d.151.1 is the DNaseI superfamily code

<sup>3</sup>Enzyme commission classification number

Figure 9C

PDB <sup>1</sup>	Score in bits (fraction to the highest score)	MOLEGOS found	SCOP <sup>2</sup>	EC <sup>3</sup>	Description
1HD7	1942 (1.00)	1,2,3,4,5,6,7,8,9,10,11,12	d.151.1.1	4.2.99.18	APE (Mn/Mg/Pb)
1AKO	1831 (0.94)	1,2,3,5,6,7,8,9,10,11,12	d.151.1.1	3.1.11.2	Exonuclease III
2DNJ	1072 (0.55)	1,2,5,6,7,9,10,12	d.151.1.1	3.1.21.1	Deoxyribonuclease I
1I9Y	971 (0.50)	1,2,5,6,7,9,10,12	d.151.1.2		Phosphatidylinositol phosphate Synaptotjanin
1QQ9	698 (0.36)	5,6,9,10,12	c.56.5.4	3.4.11.-	Aminopeptidase (Zn, Ca)
1ATL	633 (0.33)	5,6,9,10,12	d.92.1.9	3.4.24.42	Snake venom metalloprotease (Zn, Ca)
1D09	619 (0.32)	5,9,12	d.58.2.1	2.1.3.2	Aspartate carbamoyltransferase (Zn)
1D2N	613 (0.32)	5,6,8,9,12	c.37.1.13		N-ethylmaleimide of sensitive fusion protein (Mg)
1D0B	579 (0.30)	2,5,9,12	c.10.2.1		InternalinB LRR domain (Ca)
1EEM	571 (0.29)	5,6,8,12	a.45.1.1		Glutathione S-transferase

<sup>1</sup>PDB code of the protein

<sup>2</sup>SCOP code and d.151.1 is the DNaseI superfamily code

<sup>3</sup>Enzyme commission classification number

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Figure 10 - E1

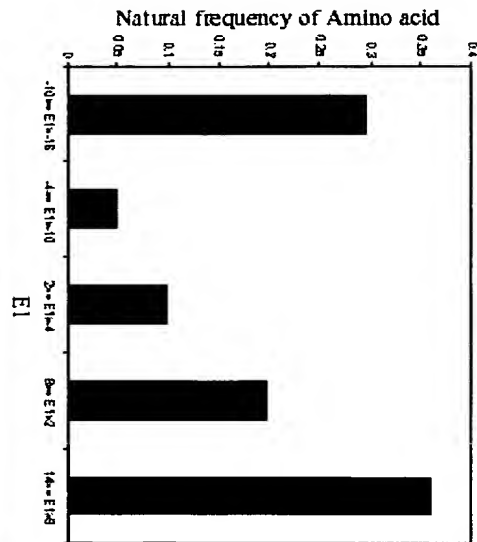


Figure 10 - E2

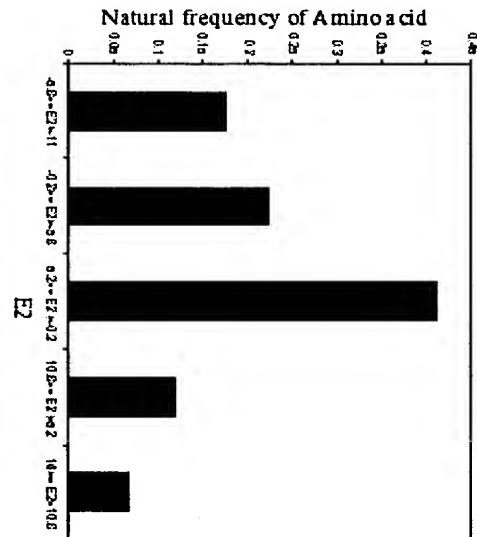


Figure 10 - E3

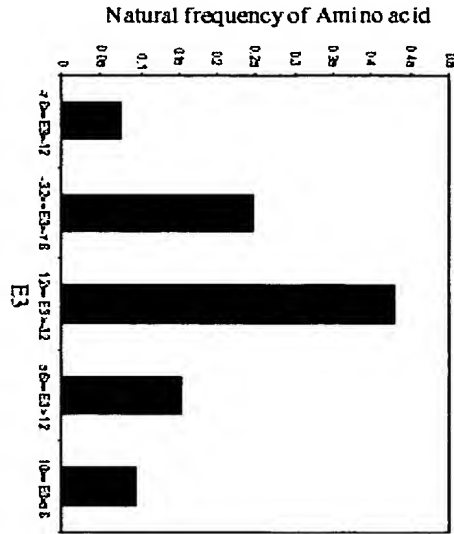


Figure 10 - E4

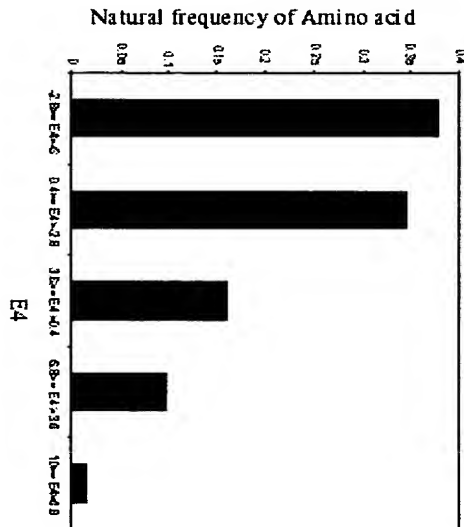


Figure 11

SEQ ID NO: 1	P	D	I	L	C	L	Q	E	T	K
E1	*	+	-	-	-	-	+	+	*	*
E2	*	-	*	*	*	*	-	-	*	-
E3	+	*	*	*	*	*	*	-	*	*
E4	*	+	*	*	+	*	+	+	*	-
E5	*	+	*	*	*	*	-	+	*	-

Figure 12A

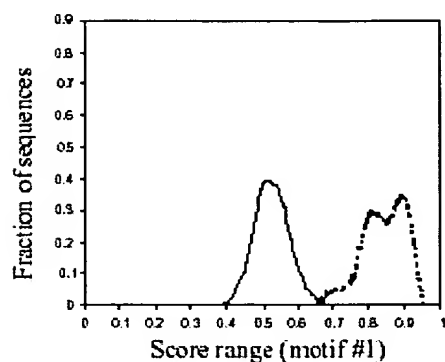


Figure 12B

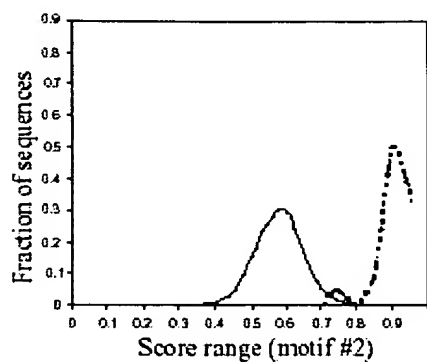


Figure 12C

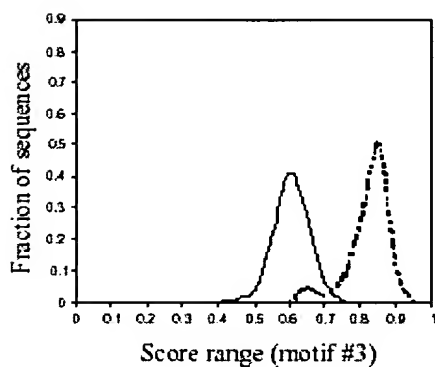


Figure 12D

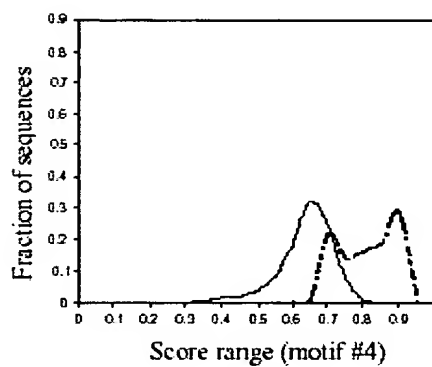


Figure 12E

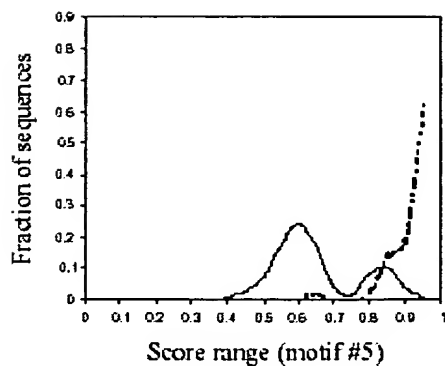


Figure 12F

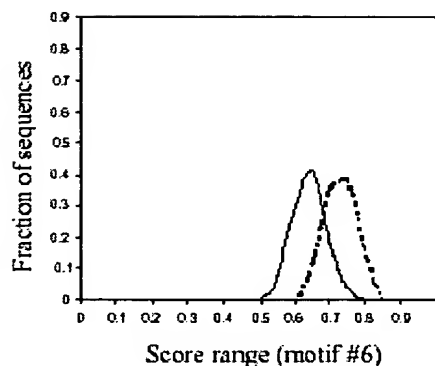


Figure 12G

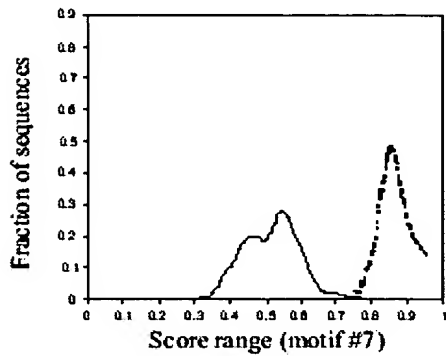


Figure 12H

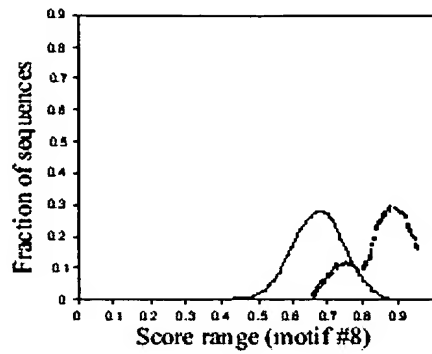


Figure 12I

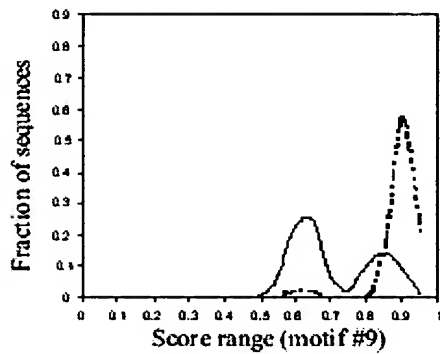


Figure 12J

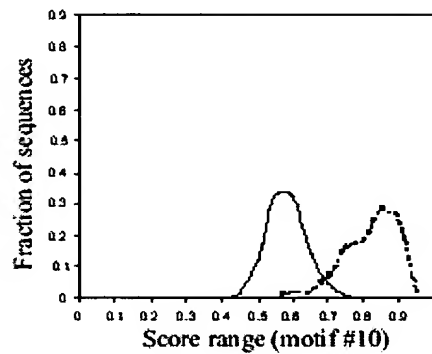


Figure 12K

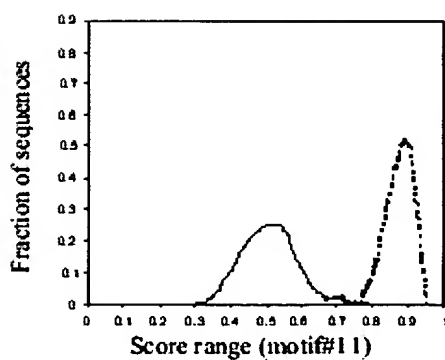


Figure 12L

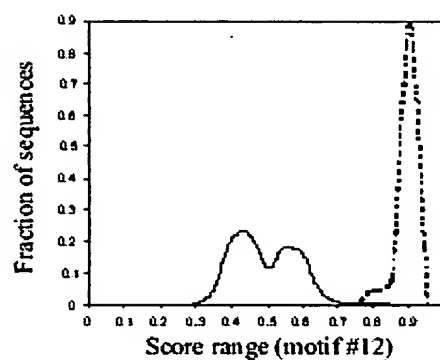


Figure 13

Seq ID No: 2	lbix	.....LYEDPPDQKTSPSGKPAT	<u>1</u>	<u>LKICSWNVDGLRAW</u>	.....IKKKGLDWVKE.EA
Seq ID No: 3	lako	.....		<u>MKEVSFNINGLRAR</u>	.....P..HOLEAIVEkHQ
Seq ID No: 4	3dni	.....		<u>LKIAAFNIRTFGe</u>	tkmsnatLASIVIRVR...R
Seq ID No: 5	li9yA	ydpiheyvnhelrkrenefseHKNVK		<u>LFVASYNLNG..CS</u>	.....ATTK.LENWLF.Pe

		<u>2</u>			
1bix		<u>P.....DILCLOETK</u>		.....CSENKL.P..AELQEL	.....PGLSHQYWS.APSD
1ako		<u>P.....DVIGLQETK</u>		.....VHDDMF.P.lEEVAKL	.....G..YNVfYH.G...
3dni		<u>Y.....DIVLIQEV</u>		.....DSHLVAvg..KLLDYL	.....nqddpNTYH.YVVSepLGR
li9yA		<u>ntpladiYVVGFOEIV</u>		qltsADPAkreweSCVKRLlngkctsgpgYVQLRSGQL.V...	

		<u>3</u>		<u>4</u>	
1bix		<u>KEGYSGVGLLSR...QCP</u>		.....LKVSYGIGDE...EHDQE	<u>GRVIVAEFD</u> .....
1ako		<u>QKGHYGVALLTK...ETP</u>		.....IAVRGFPGD...DEEAqRRIIMAEIP	...sl
3dni		<u>nSYKERYLFLFRpnkVSV</u>		.....LDTYQ.YDDGccgnDSFSR	..EPAVVKFSshstk
li9yA		.....GTALMIF...CkesclpsiknVEGTVKK		.....tGLGN.KGAVAIRFD	...ye

		<u>5</u>		<u>6</u>	
1bix		<u>..SFVLVTAYVPNAGRGLV..RLEYRQRWDEAFRKF</u>		LA...S.RK.	<u>PLVL</u>
1ako		<u>lgNVTVINGYFPQGESRDHpiKFP</u>		AKAQFYQNLQNYLET	.....EL...KrDN.
3dni		<u>vkEFAIVALHSAPS</u>		.....DAVAEINSLYDVYLD	.....VQqkwh.LN.DVMI
li9yA		<u>dtGLCFITSHLAAGY</u>		.....TNYDERDHDYRTIASglrfrgrSI	...F.NHdYVW

		<u>7</u>		<u>8</u>	
1bix		<u>CGDLNVAHEEIDLRN</u>		.....PKGKN..KNAGFTPO	.....EROGF
1ako		<u>MGDMNISFTDLDIGI</u>		geenRKRWLrtGKCSFLPE	.....EREWM
3dni		<u>MGDFNAD</u>		.....CSYVTSS	.....QWSS.
li9yA		<u>FGDFNY</u>		.....RISLtyeevvpaciaqgklsylfeydqLNKQM	

		<u>9</u>		<u>10</u>		<u>11</u>
1bix		<u>G..ELLQAVPLADSEFRHLYPNT</u>		PYAYTFWTY..MMNARSKNV...GWRLDYFLLSHS		<u>LL</u>
1ako		<u>D..RLMSW.GLVD</u>		TFRHPQTADRFSWFDY..RSKGFDDNR...GLRIDLLLASQP		<u>LA</u>
3dni		<u>I..RLRTSSTFQWLIP</u>		.....dSADTTAT	.....ST...NCAYDRIVVAGS	<u>ILQ</u>
li9yA		<u>LtgKVFP..FFSELPI</u>		.....tfPPTYKFDigTDIYDTSdkhrvPAWTDRILYRGE		<u>L.</u>

				<u>12</u>	
1bix		PALC..DSKIRSKA		.....L..... <u>GSDHCPT</u>	ITLYLAL
1ako		ECCV..ETGIDYEI		.....Rsmek	<u>PSDHAPV</u> WATFRR
3dni		SSVVpgSAAPFDFQaayglsnemala		.....ISDHYPVEVTLT	.....
li9yA		.VPH..SYQSV.PL		.....Y	<u>YSDHRPT</u> IYATYEAnivkvdrekkilfeel

1bix	.....
1ako	.....
3dni	.....
li9yA	ynqrkqevrdsq



Figure 14

